

095-US1 sequ lstg.ST25.txt
SEQUENCE LISTING

<110> Sylvia G. Kachalsky, Alexander Faerman and Yehuda Peł-Or

<120> STR50 and uses thereof

<130> 67656-A;095/US1

<140>

<141> Herewith

<150> 60/393251

<151> 2002-07-01

<160> 4

<170> PatentIn version 3.2

<210> 1

<211> 4623

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (644)..(3109)

<220>

<221> misc_feature

<222> (4250)..(4250)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (4292)..(4292)

<223> n is a, c, g, or t

<220>

<221> misc_feature

<222> (4295)..(4295)

<223> n is a, c, g, or t

<400> 1

gggcctccctg cacaatgcg ttgggtgatg ggggctgaat ccagcccaca ctgcacttgc 60

caagccagct ggggcccctgg cacaagacag tcccagccctg ttttcaactga ctttgcta 120

tctcacggag gcaccatgtg gtgtggaaag gcccggctcg cgtaacctct ctgctccag 180

gtccctgacc agtccttaac acacagtggc ctttgctcac ctgcggccca gctctggct 240

ctccccacag catccttgc cttgcctccc tcccatcttc ctctggccct tctctctgt 300

cctgcccagg aaactgtgct ctcaggagcg caggagccag ctctcagccc ccatctcctg 360

ggcactcacc gtactcagga aatatgttct gaattcagga ttatcctcat tctactgaga 420

agacctggag gacagaaatc agcaagacct aaaggggaga ggaaggaggg ccaggctggg 480

gtggaggtgc cccacccggg agcccccggcg cagcctcacc gcaggctgat tcacagaagg 540

ctcaagagggt tgcgagggcc caatcggcac tgtcatcctg cccaggctct gagtcaccag 600

095-US1 sequ lstg.ST25.txt

ctggtgaggg gcagctgcag cccagcagga aacaaagtct	agc atg gaa gag gtg	655
	Met Glu Glu Val	
	1	
gga ggg agg tgg tgg ggc ctg aaa ccc cgc ctg	gct ggc ctt aga gga	703
Gly Gly Arg Trp Trp Gly Leu Lys Pro Arg	Leu Ala Gly Leu Arg Gly	
5 10	15 20	
act ggg agt gac tgt ccg gca ctg gct cag cag	caa aca gct ctc aag	751
Thr Gly Ser Asp Cys Pro Ala Leu Ala Gln	Gln Gln Thr Ala Leu Lys	
25	30 35	
gac gtg cta gga gtc agg aac tgg gcc agc tcc	ggt ccc ttc ctt ttg	799
Asp Val Leu Gly Val Arg Asn Trp Ala Ser Ser	Gly Pro Phe Leu Leu	
40	45 50	
ggg ctc tca ctc tgg agg atg ggg tgg atg gga	ggt cag agg agc acc	847
Gly Leu Ser Leu Trp Arg Met Gly Trp Met Gly	Gly Gln Arg Ser Thr	
55	60 65	
agc cta tgg ccc tgg aca cct ggg gta ttc	agc gag ttc ctg gag gac	895
Ser Leu Trp Pro Trp Thr Pro Gly Val Phe Ser	Glu Phe Leu Glu Asp	
70	75 80	
ggt ggg atg ggg ctg tgg ttc cag caa gaa	aaa acc ggg aag atc ctg	943
Gly Gly Met Gly Leu Trp Phe Gln Gln Glu	Lys Thr Gly Lys Ile Leu	
85 90	95 100	
acg gag ttc ctc cag ttc tat gaa gac cag	tat ggc gtg gct ctc ttc	991
Thr Glu Phe Leu Gln Phe Tyr Glu Asp Gln	Tyr Gly Val Ala Leu Phe	
105	110 115	
aac agc atg cgc cat gag att gag ggc acg	ggg ctg ccg cag gcc cag	1039
Asn Ser Met Arg His Glu Ile Glu Gly Thr	Gly Leu Pro Gln Ala Gln	
120	125 130	
ctg ctc tgg cgc aag gtg cca ctg gac	gag cgc atc gtc ttc tcg	1087
Leu Leu Trp Arg Lys Val Pro Leu Asp Glu	Arg Ile Val Phe Ser Gly	
135	140 145	
aac ctc ttc cag cac cag gag gac	agc aag aag tgg aga aac cgc ttc	1135
Asn Leu Phe Gln His Gln Glu Asp Ser Lys	Lys Trp Arg Asn Arg Phe	
150	155 160	
agc ctc gtg ccc cac aac tac ggg ctg	gtg ctc tac gaa aac aaa gcg	1183
Ser Leu Val Pro His Asn Tyr Gly Leu Val	Leu Tyr Glu Asn Lys Ala	
165	170 175 180	
gcc tat gag cgg cag gtc cca cca cga	gcc gtc atc aac agt gca ggc	1231
Ala Tyr Glu Arg Gln Val Pro Pro Arg Ala	Val Ile Asn Ser Ala Gly	
185	190 195	
tac aaa atc ctc acg tcc gtg gac caa	tac ctg gag ctc att ggc aac	1279
Tyr Lys Ile Leu Thr Ser Val Asp Gln	Tyr Leu Glu Leu Ile Gly Asn	
200	205 210	
tcc tta cca ggg acc acg gca aag tcg	ggc agt gcc ccc atc ctc aag	1327
Ser Leu Pro Gly Thr Thr Ala Lys Ser Gly	Ser Ala Pro Ile Leu Lys	
215	220 225	
tgc ccc aca cag ttc ccg ctc atc ctc tgg	cat cct tat gcg cgt cac	1375
Cys Pro Thr Gln Phe Pro Leu Ile Leu Trp	His Pro Tyr Ala Arg His	
230	235 240	

095-US1 sequ lstg.ST25.txt

tac tac ttc tgc atg atg aca gaa gcc gag cag gac aag tgg cag gct Tyr Tyr Phe Cys Met Met Thr Glu Ala Glu Gln Asp Lys Trp Gln Ala 245 250 255 260	1423
gtg ctg cag gac tgc atc cgg cac tgc aac aat gga atc cct gag gac Val Leu Gln Asp Cys Ile Arg His Cys Asn Asn Gly Ile Pro Glu Asp 265 270 275	1471
tcc aag gta gag ggc cct gcg ttc aca gat gcc atc cgc atg tac cga Ser Lys Val Glu Gly Pro Ala Phe Thr Asp Ala Ile Arg Met Tyr Arg 280 285 290	1519
cag tcc aag gag ctg tac ggc acc tgg gag atg ctg tgt ggg aac gag Gln Ser Lys Glu Leu Tyr Gly Thr Trp Glu Met Leu Cys Gly Asn Glu 295 300 305	1567
gtg cag atc ctg agc aac ctg gtg atg gag gag ctg ggc cct gag ctg Val Gln Ile Leu Ser Asn Leu Val Met Glu Leu Gly Pro Glu Leu 310 315 320	1615
aag gca gag ctc ggc ccg cgg ctg aag ggg aaa ccg cag gag cgg cag Lys Ala Glu Leu Gly Pro Arg Leu Lys Gly Lys Pro Gln Glu Arg Gln 325 330 335 340	1663
cgg cag tgg atc cag atc tcg gac gcc gtg tac cac atg gtg tac gag Arg Gln Trp Ile Gln Ile Ser Asp Ala Val Tyr His Met Val Tyr Glu 345 350 355	1711
cag gcc aag gcg cgc ttc gag gag gtg ctg tcc aag gtg cag cag gtg Gln Ala Lys Ala Arg Phe Glu Glu Val Leu Ser Lys Val Gln Gln Val 360 365 370	1759
cag ccg gcc atg cag gcc gtc atc cga act gac atg gac caa att atc Gln Pro Ala Met Gln Ala Val Ile Arg Thr Asp Met Asp Gln Ile Ile 375 380 385	1807
acc tcc aag gag cac ctt gcc agc aag atc cga gcc ttc atc ctc ccc Thr Ser Lys Glu His Leu Ala Ser Lys Ile Arg Ala Phe Ile Leu Pro 390 395 400	1855
aag gca gag gtg tgc gtg cgg aac cat gtc cag ccc tac atc cca tcc Lys Ala Glu Val Cys Val Arg Asn His Val Gln Pro Tyr Ile Pro Ser 405 410 415 420	1903
atc ctg gag gcc ctg atg gtc ccc acc agc cag ggc ttc act gag gtg Ile Leu Glu Ala Leu Met Val Pro Thr Ser Gln Gly Phe Thr Glu Val 425 430 435	1951
cga gat gtc ttc ttc aag gag gtc acg gac atg aac ctg aac gtc atc Arg Asp Val Phe Phe Lys Glu Val Thr Asp Met Asn Leu Asn Val Ile 440 445 450	1999
aac gag ggc att gac aag ctg ggc gag tac atg gag aag ctg tcc Asn Glu Gly Gly Ile Asp Lys Leu Gly Glu Tyr Met Glu Lys Leu Ser 455 460 465	2047
cgg ctg gcg tac cac ccc ctg aag atg cag agc tgc tat gag aag atg Arg Leu Ala Tyr His Pro Leu Lys Met Gln Ser Cys Tyr Glu Lys Met 470 475 480	2095
gag tcg ctg cga ctg gac ggg ctg cag cag cga ttt gat gtg tcc agc Glu Ser Leu Arg Leu Asp Gly Leu Gln Gln Arg Phe Asp Val Ser Ser 485 490 495 500	2143

095-US1 sequ lstg.ST25.txt

acg tcc gtg ttc aag cag cga gcc cag atc cac atg cg ^g gag caa atg Thr Ser Val Phe Lys Gln Arg Ala Gln Ile His Met Arg Glu Gln Met 505 510 515	2191
gac aat gcc gtg tat acg ttc gag acc ctc ctg cac cag gag ctg ggg Asp Asn Ala Val Tyr Thr Phe Glu Thr Leu Leu His Gln Glu Leu Gly 520 525 530	2239
aag ggg ccc acc aag gag gag ctg tgc aag tcc atc cag cgg gtc ctg Lys Gly Pro Thr Lys Glu Glu Leu Cys Lys Ser Ile Gln Arg Val Leu 535 540 545	2287
gag cgg gtg ctg aaa aaa tac gac tac gac agc agc tct gtg cgg aag Glu Arg Val Leu Lys Lys Tyr Asp Tyr Asp Ser Ser Val Arg Lys 550 555 560	2335
, agg ttc ttc cgg gag gcg ctg ctg cag atc agc atc ccg ttc ctg ctc Arg Phe Arg Glu Ala Leu Leu Gln Ile Ser Ile Pro Phe Leu Leu 565 570 575 580	2383
aag aag ctg gcc cct acc tgc aag tcg gag ctg ccc cgg ttc cag gag Lys Lys Leu Ala Pro Thr Cys Lys Ser Glu Leu Pro Arg Phe Gln Glu 585 590 595	2431
ctg atc ttc gag gac ttt gcc agg ttc atc ctg gtg gaa aac acg tac Leu Ile Phe Glu Asp Phe Ala Arg Phe Ile Leu Val Glu Asn Thr Tyr 600 605 610	2479
gag gag gtg gtg ctg cag acc gtc atg aag gac atc ctg cag gct gtg Glu Glu Val Val Leu Gln Thr Val Met Lys Asp Ile Leu Gln Ala Val 615 620 625	2527
aag gag gcc gcg gtg cag agg aag cac aac ctc tac ccg gac agc atg Lys Glu Ala Ala Val Gln Arg Lys His Asn Leu Tyr Arg Asp Ser Met 630 635 640	2575
gtc atg cac aac agc gac ccc aac ctg cac ctg ctg gcc gag ggc gcc Val Met His Asn Ser Asp Pro Asn Leu His Leu Ala Glu Gly Ala 645 650 655 660	2623
ccc atc gac tgg ggc gag gag tac agc aac agc ggc ggg ggc ggc agc Pro Ile Asp Trp Gly Glu Glu Tyr Ser Asn Ser Gly Gly Gly Ser 665 670 675	2671
ccc agc ccc agc acc ccg gag tca gcc acc ctc tcg gaa aag cga cgg Pro Ser Pro Ser Thr Pro Glu Ser Ala Thr Leu Ser Glu Lys Arg Arg 680 685 690	2719
cgc gcc aag cag gtg gtc tct gtg gtc cag gat gag gag gtg ggg ctg Arg Ala Lys Gln Val Val Ser Val Val Gln Asp Glu Glu Val Gly Leu 695 700 705	2767
ccc ttt gag gct agc cct gag tca cca cca cct gcg tcc ccg gac ggt Pro Phe Glu Ala Ser Pro Glu Ser Pro Pro Pro Ala Ser Pro Asp Gly 710 715 720	2815
gtc act gag atc cga ggc ctg ctg gcc caa ggt ctg cgg cct gag agc Val Thr Glu Ile Arg Gly Leu Leu Ala Gln Gly Leu Arg Pro Glu Ser 725 730 735 740	2863
ccc cca cca gcc ggc ccc ctg ctc aac ggg gcc ccc gct ggg gag agt Pro Pro Pro Ala Gly Pro Leu Leu Asn Gly Ala Pro Ala Gly Glu Ser 745 750 755	2911

095-US1 sequ 1stg.ST25.txt

ccc cag cct aag gcc gcc ccc gag gcc tcc tcg ccg cct gcc tca ccc Pro Gln Pro Lys Ala Ala Pro Glu Ala Ser Ser Pro Pro Ala Ser Pro 760 765 770	2959
ctc cag cat ctc ctg cct gga aag gct gtg gac ctt ggg ccc ccc aag Leu Gln His Leu Leu Pro Gly Lys Ala Val Asp Leu Gly Pro Pro Lys 775 780 785	3007
ccc agc gac cag gag act gga gag cag gtg tcc agc ccc agc agc cac Pro Ser Asp Gln Glu Thr Gly Glu Gln Val Ser Ser Pro Ser Ser His 790 795 800	3055
ccc gcc ctc cac acc acc gag gac agt gca ggg gtg cag act gag Pro Ala Leu His Thr Thr Glu Asp Ser Ala Gly Val Gln Thr Glu 805 810 815 820	3103
ttc tag gccagtgggt ccctgactgc tgcacatggc acaggccgtt cccttccgga Phe	3159
cccaggcagg ctcagctctg gggagggcac cctggcttgt gccttgtggg tggaggcggg gcagggctgt gtggcaccgc cagggagcgg gcccacctga gtcactttat tgggttcagt caacactttc ttgctccctg tttctcttc tgtggatga tctcagatgc aggggctggt tttggggtt tcctgcttgt gccaagggtt ggacactgtt gggggctgg aaagcccctc ccttcctgtc cttctgtggc ctccatcccc tcatgggtgc tgccatcctt cctggagaga gggaggtgaa agctggtgtg agcccagtgg gttccccc actcaccagg gagctggctg ggccaggacc gggagagggc gcactgctgc cctcctggcc ctgctcccttc cgcagtagg ggtgaccga gcctcgctt cccactgtt ctggaggaa gggaaaggag ggggtcttca ggctggagcc aggctggggg tgctgggtgg agagatgaga tttaggggt gcctcatggg gtggcaggg ctgggtgaa atgagaaagg cccagaacgt gcaggtctgc ggagggaaag tgtcctgagt gaaggagggg accccatctt gggatgtt gtagtgagtg agtgagatgg ctgagtgagg gttatggggc gcctgaggtt ttatggcct gtgtatcccc ttctccggc cccagcctgc ctccctcctg cccgcctggc ccacaggctt ccctctggc cctgtccctc tgtgggtgg gatggagcg gcagcaaggg gtgtatggg gctgggtct gtcttctaca ggccaccccg aggtcctcag tgggtgcctg gggagccggc cggggctctt gaggggtaca ggttgggtgg gcctccctg agggctgtgg gtcaggctt ggctctgtt gcctctcagt caccaagtca cttccctctg aaaatccagt ccctcttgc gatgtccttg tgagtca tggccctggc tgctcgctt ctcagcttc ttgttgcctg gacaagggtc aagccaggat ggcccccaggc ntggatccc ccacccagg accccacagg cccctcccc tgntgnnttgc cggggggcag ggcagaaatg gactcctttt gggcccccga ggtgggtcc cctccagcc ctgcattcctc cgtgccttag acctgctccc cagaggaggg gccttgacc acaggaagtgc tggtggcgcc tggcaatcag ggaccccccag ctgccgcagc cctggttttt ggccatctt	3219 3279 3339 3399 3459 3519 3579 3639 3699 3759 3819 3879 3939 3999 4059 4119 4179 4239 4299 4359 4419 4479

095-US1 sequ 1stg.ST25.txt
ttcccttgc tccccagat ttgcgcctt agtgccttt gaggggttcc catcatccct 4539
ccctgatatt gtattgaaaa tattatgcac actgttcatg ctttactaa tcaataaacg 4599
ctttatcaa aaaaaaaaaaaa aaaa 4623

<210> 2
<211> 821
<212> PRT
<213> Homo sapiens

<400> 2

Met Glu Glu Val Gly Gly Arg Trp Trp Gly Leu Lys Pro Arg Leu Ala
1 5 10 15

Gly Leu Arg Gly Thr Gly Ser Asp Cys Pro Ala Leu Ala Gln Gln Gln
20 25 30

Thr Ala Leu Lys Asp Val Leu Gly Val Arg Asn Trp Ala Ser Ser Gly
35 40 45

Pro Phe Leu Leu Gly Leu Ser Leu Trp Arg Met Gly Trp Met Gly Gly
50 55 60

Gln Arg Ser Thr Ser Leu Trp Pro Trp Thr Pro Gly Val Phe Ser Glu
65 70 75 80

Phe Leu Glu Asp Gly Gly Met Gly Leu Trp Phe Gln Gln Glu Lys Thr
85 90 95

Gly Lys Ile Leu Thr Glu Phe Leu Gln Phe Tyr Glu Asp Gln Tyr Gly
100 105 110

Val Ala Leu Phe Asn Ser Met Arg His Glu Ile Glu Gly Thr Gly Leu
115 120 125

Pro Gln Ala Gln Leu Leu Trp Arg Lys Val Pro Leu Asp Glu Arg Ile
130 135 140

Val Phe Ser Gly Asn Leu Phe Gln His Gln Glu Asp Ser Lys Lys Trp
145 150 155 160

Arg Asn Arg Phe Ser Leu Val Pro His Asn Tyr Gly Leu Val Leu Tyr
165 170 175

Glu Asn Lys Ala Ala Tyr Glu Arg Gln Val Pro Pro Arg Ala Val Ile
180 185 190

Asn Ser Ala Gly Tyr Lys Ile Leu Thr Ser Val Asp Gln Tyr Leu Glu
195 200 205

095-US1 sequ 1stg.ST25.txt

Leu Ile Gly Asn Ser Leu Pro Gly Thr Thr Ala Lys Ser Gly Ser Ala
210 215 220

Pro Ile Leu Lys Cys Pro Thr Gln Phe Pro Leu Ile Leu Trp His Pro
225 230 235 240

Tyr Ala Arg His Tyr Tyr Phe Cys Met Met Thr Glu Ala Glu Gln Asp
245 250 255

Lys Trp Gln Ala Val Leu Gln Asp Cys Ile Arg His Cys Asn Asn Gly
260 265 270

Ile Pro Glu Asp Ser Lys Val Glu Gly Pro Ala Phe Thr Asp Ala Ile
275 280 285

Arg Met Tyr Arg Gln Ser Lys Glu Leu Tyr Gly Thr Trp Glu Met Leu
290 295 300

Cys Gly Asn Glu Val Gln Ile Leu Ser Asn Leu Val Met Glu Glu Leu
305 310 315 320

Gly Pro Glu Leu Lys Ala Glu Leu Gly Pro Arg Leu Lys Gly Lys Pro
325 330 335

Gln Glu Arg Gln Arg Gln Trp Ile Gln Ile Ser Asp Ala Val Tyr His
340 345 350

Met Val Tyr Glu Gln Ala Lys Ala Arg Phe Glu Glu Val Leu Ser Lys
355 360 365

Val Gln Gln Val Gln Pro Ala Met Gln Ala Val Ile Arg Thr Asp Met
370 375 380

Asp Gln Ile Ile Thr Ser Lys Glu His Leu Ala Ser Lys Ile Arg Ala
385 390 395 400

Phe Ile Leu Pro Lys Ala Glu Val Cys Val Arg Asn His Val Gln Pro
405 410 415

Tyr Ile Pro Ser Ile Leu Glu Ala Leu Met Val Pro Thr Ser Gln Gly
420 425 430

Phe Thr Glu Val Arg Asp Val Phe Phe Lys Glu Val Thr Asp Met Asn
435 440 445

Leu Asn Val Ile Asn Glu Gly Gly Ile Asp Lys Leu Gly Glu Tyr Met
450 455 460

095-US1 sequ 1stg.ST25.txt

Glu Lys Leu Ser Arg Leu Ala Tyr His Pro Leu Lys Met Gln Ser Cys
465 470 475 480

Tyr Glu Lys Met Glu Ser Leu Arg Leu Asp Gly Leu Gln Gln Arg Phe
485 490 495

Asp Val Ser Ser Thr Ser Val Phe Lys Gln Arg Ala Gln Ile His Met
500 505 510

Arg Glu Gln Met Asp Asn Ala Val Tyr Thr Phe Glu Thr Leu Leu His
515 520 525

Gln Glu Leu Gly Lys Gly Pro Thr Lys Glu Glu Leu Cys Lys Ser Ile
530 535 540

Gln Arg Val Leu Glu Arg Val Leu Lys Lys Tyr Asp Tyr Asp Ser Ser
545 550 555 560

Ser Val Arg Lys Arg Phe Phe Arg Glu Ala Leu Leu Gln Ile Ser Ile
565 570 575

Pro Phe Leu Leu Lys Lys Leu Ala Pro Thr Cys Lys Ser Glu Leu Pro
580 585 590

Arg Phe Gln Glu Leu Ile Phe Glu Asp Phe Ala Arg Phe Ile Leu Val
595 600 605

Glu Asn Thr Tyr Glu Glu Val Val Leu Gln Thr Val Val Met Lys Asp Ile
610 615 620

Leu Gln Ala Val Lys Glu Ala Ala Val Gln Arg Lys His Asn Leu Tyr
625 630 635 640

Arg Asp Ser Met Val Met His Asn Ser Asp Pro Asn Leu His Leu Leu
645 650 655

Ala Glu Gly Ala Pro Ile Asp Trp Gly Glu Glu Tyr Ser Asn Ser Gly
660 665 670

Gly Gly Gly Ser Pro Ser Pro Ser Thr Pro Glu Ser Ala Thr Leu Ser
675 680 685

Glu Lys Arg Arg Arg Ala Lys Gln Val Val Ser Val Val Gln Asp Glu
690 695 700

Glu Val Gly Leu Pro Phe Glu Ala Ser Pro Glu Ser Pro Pro Pro Ala
705 710 715 720

095-US1 sequ lstg.ST25.txt

Ser Pro Asp Gly Val Thr Glu Ile Arg Gly Leu Leu Ala Gln Gly Leu
725 730 735

Arg Pro Glu Ser Pro Pro Pro Ala Gly Pro Leu Leu Asn Gly Ala Pro
740 745 750

Ala Gly Glu Ser Pro Gln Pro Lys Ala Ala Pro Glu Ala Ser Ser Pro
755 760 765

Pro Ala Ser Pro Leu Gln His Leu Leu Pro Gly Lys Ala Val Asp Leu
770 775 780

Gly Pro Pro Lys Pro Ser Asp Gln Glu Thr Gly Glu Gln Val Ser Ser
785 790 795 800

Pro Ser Ser His Pro Ala Leu His Thr Thr Glu Asp Ser Ala Gly
805 810 815

Val Gln Thr Glu Phe
820

<210> 3
<211> 4533
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (644)..(3019)

<220>
<221> misc feature
<222> (4160)..(4160)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (4202)..(4202)
<223> n is a, c, g, or t

<220>
<221> misc_feature
<222> (4205)..(4205)
<223> n is a, c, g, or t

<400> 3
gggcctccctg cacaaatgcg ttgggtgatg ggggctgaat ccagcccaca ctgcacttgc 60
caagccagct ggggccttg cacaagacag tcccgccctg ttttcactga ctttgcta 120
tctcacggag gcaccatgtg gtgtggaaag gcccggctt cgtaacctct ctgctcccc 180
gtccctgacc agtccttaac acacagtggt ctttgctcac ctgcggccca gctctggc 240

095-US1 sequ lstg.ST25.txt

ctccccacag catccttgc ctgcctccc tcccatttc ctctggccct tctctgtct	300
cctggccagg aaactgtgct ctcaggagcg caggagccag ctctcagccc ccatctcctg	360
ggcactcacc gtactcagga aatatgttct gaattcagga ttatcctcat tctactgaga	420
agacctggag gacagaaatc agcaagacct aaaggggaga ggaaggaggg ccaggctggg	480
gtggagggtgc cccacccggg agcccgccg cagcctcacc gcaggctgat tcacagaagg	540
ctcagagggt tgcgagggcc caatcggcac tgtcatcctg cccaggctct gagtcaccag	600
ctggtgaggg gcagctgcag cccagcagga aacaaagtct agc atg gaa gag gtg Met Glu Glu Val 1	655
 gga ggg agg tgg tgg ggc ctg aaa ccc cgc ctg gct ggc ctt aga gga Gly Gly Arg Trp Trp Gly Leu Lys Pro Arg Leu Ala Gly Leu Arg Gly 5 10 15 20	703
act ggg agt gac tgt ccg gca ctg gct cag cag caa aca gct ctc aag Thr Gly Ser Asp Cys Pro Ala Leu Ala Gln Gln Thr Ala Leu Lys 25 30 35	751
gac gtg cta gga gtc agg aac tgg gcc agc tcc ggt ccc ttc ctt ttg Asp Val Leu Gly Val Arg Asn Trp Ala Ser Ser Gly Pro Phe Leu Leu 40 45 50	799
ggg ctc tca ctc tgg agg atg ggg tgg atg gga gaa aaa acc ggg aag Gly Leu Ser Leu Trp Arg Met Gly Trp Met Gly Glu Lys Thr Gly Lys 55 60 65	847
atc ctg acg gag ttc ctc cag ttc tat gaa gac cag tat ggc gtg gct Ile Leu Thr Glu Phe Leu Gln Phe Tyr Glu Asp Gln Tyr Gly Val Ala 70 75 80	895
ctc ttc aac agc atg cgc cat gag att gag ggc acg ggg ctg ccg cag Leu Phe Asn Ser Met Arg His Glu Ile Glu Gly Thr Gly Leu Pro Gln 85 90 95 { 100	943
gcc cag ctg ctc tgg cgc aag gtg cca ctg gac gag cgc atc gtc ttc Ala Gln Leu Leu Trp Arg Lys Val Pro Leu Asp Glu Arg Ile Val Phe 105 110 115	991
tcg ggg aac ctc ttc cag cac cag gag gac agc aag aag tgg aga aac Ser Gly Asn Leu Phe Gln His Gln Glu Asp Ser Lys Lys Trp Arg Asn 120 125 130	1039
cgc ttc agc ctc gtg ccc cac aac tac ggg ctg gtg ctc tac gaa aac Arg Phe Ser Leu Val Pro His Asn Tyr Gly Leu Val Leu Tyr Glu Asn 135 140 145	1087
aaa gcg gcc tat gag cgg cag gtc cca cca cga gcc gtc atc aac agt Lys Ala Ala Tyr Glu Arg Gln Val Pro Pro Arg Ala Val Ile Asn Ser 150 155 160	1135
gca ggc tac aaa atc ctc acg tcc gtg gac caa tac ctg gag ctc att Ala Gly Tyr Lys Ile Leu Thr Ser Val Asp Gln Tyr Leu Glu Leu Ile 165 170 175 180	1183
ggc aac tcc tta cca ggg acc acg gca aag tcg ggc agt gcc ccc atc Gly Asn Ser Leu Pro Gly Thr Thr Ala Lys Ser Gly Ser Ala Pro Ile 185 190 195	1231

095-US1 sequ lstg.ST25.txt

ctc aag tgc ccc aca cag ttc ccg ctc atc ctc tgg cat cct tat gcg Leu Lys Cys Pro Thr Gln Phe Pro Leu Ile Leu Trp His Pro Tyr Ala 200 205 210	1279
cgt cac tac tac ttc tgc atg atg aca gaa gcc gag cag gac aag tgg Arg His Tyr Tyr Phe Cys Met Met Thr Glu Ala Glu Gln Asp Lys Trp 215 220 225	1327
cag gct gtg ctg cag gac tgc atc cgg cac tgc aac aat gga atc cct Gln Ala Val Leu Gln Asp Cys Ile Arg His Cys Asn Asn Gly Ile Pro 230 235 240	1375
gag gac tcc aag gta gag ggc cct gcg ttc aca gat gcc atc cgc atg Glu Asp Ser Lys Val Glu Gly Pro Ala Phe Thr Asp Ala Ile Arg Met 245 250 255 260	1423
tac cga cag tcc aag gag ctg tac ggc acc tgg gag atg ctg tgt ggg Tyr Arg Gln Ser Lys Glu Leu Tyr Gly Thr Trp Glu Met Leu Cys Gly 265 270 275	1471
aac gag gtg cag atc ctg agc aac ctg gtg atg gag gag ctg ggc cct Asn Glu Val Gln Ile Leu Ser Asn Leu Val Met Glu Glu Leu Gly Pro 280 285 290	1519
gag ctg aag gca gag ctc ggc ccg cgg ctg aag ggg aaa ccg cag gag Glu Leu Lys Ala Glu Leu Gly Pro Arg Leu Lys Gly Lys Pro Gln Glu 295 300 305	1567
cg ^g cag cg ^g cag tgg atc cag atc tcg gac gcc gtg tac cac atg gtg Arg Gln Arg Gln Trp Ile Gln Ile Ser Asp Ala Val Tyr His Met Val 310 315 320	1615
tac gag cag gcc aag gc ^g cgc ttc gag gag gtg ctg tcc aag gtg cag Tyr Glu Gln Ala Lys Ala Arg Phe Glu Glu Val Leu Ser Lys Val Gln 325 330 335 340	1663
cag gtg cag cc ^g gcc atg cag gcc gtc atc cga act gac atg gac caa Gln Val Gln Pro Ala Met Gln Ala Val Ile Arg Thr Asp Met Asp Gln 345 350 355	1711
att atc acc tcc aag gag cac ctt gcc agc aag atc cga gcc ttc atc Ile Ile Thr Ser Lys Glu His Leu Ala Ser Lys Ile Arg Ala Phe Ile 360 365 370	1759
ctc ccc aag gca gag gtg tgc gtg cgg aac cat gtc cag ccc tac atc Leu Pro Lys Ala Glu Val Cys Val Arg Asn His Val Gln Pro Tyr Ile 375 380 385	1807
cca tcc atc ctg gag gcc ctg atg gtc ccc acc agc cag ggc ttc act Pro Ser Ile Leu Glu Ala Leu Met Val Pro Thr Ser Gln Gly Phe Thr 390 395 400	1855
gag gtg cga gat gtc ttc aag gag gtc acg gac atg aac ctg aac Glu Val Arg Asp Val Phe Phe Lys Glu Val Thr Asp Met Asn Leu Asn 405 410 415 420	1903
gtc atc aac gag ggc ggc att gac aag ctg ggc gag tac atg gag aag Val Ile Asn Glu Gly Ile Asp Lys Leu Gly Glu Tyr Met Glu Lys 425 430 435	1951
ctg tcc cgg ctg gc ^g tac cac ccc ctg aag atg cag agc tgc tat gag Leu Ser Arg Leu Ala Tyr His Pro Leu Lys Met Gln Ser Cys. Tyr Glu 440 445 450	1999

095-US1 sequ 1stg.ST25.txt

aag atg gag tcg ctg cga ctg gac ggg ctg cag cag cga ttt gat gtg Lys Met Glu Ser Leu Arg Leu Asp Gly Leu Gln Gln Arg Phe Asp Val 455 460 465	2047
tcc acg acg tcc gtg ttc aag cag cga gcc cag atc cac atc cggtt Ser Ser Thr Ser Val Phe Lys Gln Arg Ala Gln Ile His Met Arg Glu 470 475 480	2095
caa atg gac aat gcc gtg tat acg ttc gag acc ctc ctg cac cag gag Gln Met Asp Asn Ala Val Tyr Thr Phe Glu Thr Leu Leu His Gln Glu 485 490 495 500	2143
ctg ggg aag ggg ccc acc aag gag gag ctg tgc aag tcc atc cag cggtt Leu Gly Lys Gly Pro Thr Lys Glu Leu Cys Lys Ser Ile Gln Arg 505 510 515	2191
gtc ctg gag cggtt ctg aaa aaa tac gac tac gac agc agc tct gtg Val Leu Glu Arg Val Leu Lys Lys Tyr Asp Tyr Asp Ser Ser Val 520 525 530	2239
cgg aag agg ttc ttc cgg gag gcg ctg ctg cag atc agc atc ccgtt Arg Lys Arg Phe Phe Arg Glu Ala Leu Leu Gln Ile Ser Ile Pro Phe 535 540 545	2287
ctg ctc aag aag ctg gcc cct acc tgc aag tcg gag ctg ccc cggtt Leu Leu Lys Lys Leu Ala Pro Thr Cys Lys Ser Glu Leu Pro Arg Phe 550 555 560	2335
cag gag ctg atc ttc gag gac ttt gcc agg ttc atc ctg gtg gaa aac Gln Glu Leu Ile Phe Glu Asp Phe Ala Arg Phe Ile Leu Val Glu Asn 565 570 575 580	2383
acg tac gag gag gtg gtg ctg cag acc gtc atg aag gac atc ctg cag Thr Tyr Glu Glu Val Val Leu Gln Thr Val Met Lys Asp Ile Leu Gln 585 590 595	2431
gct gtg aag gag gcc gcg gtg cag agg aag cac aac ctc tac cggtt Ala Val Lys Glu Ala Ala Val Gln Arg Lys His Asn Leu Tyr Arg Asp 600 605 610	2479
agc atg gtc atg cac aac agc gac ccc aac ctg cac ctg ctg gcc gag Ser Met Val Met His Asn Ser Asp Pro Asn Leu His Leu Leu Ala Glu 615 620 625	2527
ggc gcc ccc atc gac tgg ggc gag gag tac agc aac agc ggc ggg ggc Gly Ala Pro Ile Asp Trp Gly Glu Tyr Ser Asn Ser Gly Gly Gly 630 635 640	2575
ggc agc ccc agc ccc agc acc ccgtt gag tca gcc acc ctc tcg gaa aag Gly Ser Pro Ser Pro Ser Thr Pro Glu Ser Ala Thr Leu Ser Glu Lys 645 650 655 660	2623
cga cgg cgc gcc aag cag gtg gtc tct gtg gtc cag gat gag gag gtg Arg Arg Arg Ala Lys Gln Val Val Ser Val Val Gln Asp Glu Glu Val 665 670 675	2671
ggg ctg ccc ttt gag gct agc cct gag tca cca cca cct gcg tcc ccgtt Gly Leu Pro Phe Glu Ala Ser Pro Glu Ser Pro Pro Pro Ala Ser Pro 680 685 690	2719
gac ggt gtc act gag atc cga ggc ctg ctg gcc caa ggt ctg cgg cct Asp Gly Val Thr Glu Ile Arg Gly Leu Leu Ala Gln Gly Leu Arg Pro 695 700 705	2767

095-US1 sequ 1stg.ST25.txt

gag agc ccc cca cca gcc ggc ccc ctg ctc aac ggg gcc ccc gct ggg Glu Ser Pro Pro Pro Ala Gly Pro Leu Leu Asn Gly Ala Pro Ala Gly 710 715 720	2815
gag agt ccc cag cct aag gcc gcc ccc gag gcc tcc tcg ccg cct gcc Glu Ser Pro Gln Pro Lys Ala Ala Pro Glu Ala Ser Ser Pro Pro Ala 725 730 735 740	2863
tca ccc ctc cag cat ctc ctg cct gga aag gct gtg gac ctt ggg ccc Ser Pro Leu Gln His Leu Leu Pro Gly Lys Ala Val Asp Leu Gly Pro 745 750 755	2911
ccc aag ccc agc gac cag gag act gga gag cag gtg tcc agc ccc agc Pro Lys Pro Ser Asp Gln Glu Thr Gly Glu Gln Val Ser Ser Pro Ser 760 765 770	2959
agc cac ccc gcc ctc cac acc acc gag gac agt gca ggg gtg cag Ser His Pro Ala Leu His Thr Thr Glu Asp Ser Ala Gly Val Gln 775 780 785	3007
act gag ttc tag gccagtgggt ccctgactgc tgcacatggc acaggccgtt Thr Glu Phe 790	3059
cccttccgga cccaggcagg cttagtctg gggagggcac cctggctgt gccttgtggg tggaggcggg gcagggtgt gtggcaccgc cagggagcgg gcccacctga gtcactttat tgggttcagt caacacttgc ttgctccctg tttctcttc tgtggatga tctcagatgc aggggcttgtt tttgggttt tcctgctgt gccaagggt ggacactgct gggggctgg aaagccccctc ctttcctgtc cttctgtggc ctccatcccc tcatgggtgc tgccatcatt cctgagaga gggaggtgaa agctgggtgt agcccaagtgg gttcccgccc actcacccag gagctggctg ggccaggacc gggagaggaa gcactgctgc cttctggcc ctgctccatt cgccatggg ggtggaccga gcctcgctt ccccaactgtt ctggagggaa gggaaaggag ggggcttca ggctggagcc aggctgggg tgctgggtgg agagatgaga ttttaggggt gcctcatggg gtggcaggc ctggggtgaa atgagaaaagg cccagaacgt gcaggtctgc ggagggaaag tgtcctgagt gaaggagggg accccatcct gggatgctg ggagtgagtg agtgagatgg ctgagtgagg gttatggga gcctgagggtt ttatgggcct gtgtatcccc ttctcccgcc cccagcctgc ctccctctg cccgcctggc ccacaggctc ccctctggc cctgtccctc tggtggttg ggatggagcg gcagcaaggg gtgtaatggg gctgggtct gtcttctaca ggccaccccg aggtcctcag tggttgcctg gggagccgga cggggctcct gaggggtaca ggttgggtgg gcctccctg agggtctggg gtcaggctt ggcctctgt gcctctcagt caccaagtca cttccctctg aaaatccagt cccttctttg gatgtccttg tgagtcactc tgggcctggc tgctgtccct cctcagcttc ttgttgcctg gacaagggtc aagccaggat gggcccaggc ntgggatccc ccaccccagg accccacagg ccccccctcccc tgntgntttg cggggggcag ggcagaaatg gactcctttt gggtccccga ggtgggtcc 4259	3119
	3179
	3239
	3299
	3359
	3419
	3479
	3539
	3599
	3659
	3719
	3779
	3839
	3899
	3959
	4019
	4079
	4139
	4199

095-US1 sequ 1stg.ST25.txt
cctcccaagcc ctgcatcctc cgtgccctag acctgctccc cagaggaggg gccttgaccc 4319
acaggaagtg tggtggcgcc tggcaatcag ggaccccaag ctgcccgcagc cctgggtttt 4379
ggcgcatctt ttccctcttg tcccaagat ttgcgccttt agtgcctttt gaggggttcc 4439
catcatccct ccctgatatt gtattgaaaa tattatgcac actgttcatg ctttactaa 4499
tcaataaacg ctttatttaa aaaaaaaaaa aaaa 4533

<210> 4
<211> 791
<212> PRT
<213> Homo sapiens

<400> 4

Met Glu Glu Val Gly Gly Arg Trp Trp Gly Leu Lys Pro Arg Leu Ala
1 5 10 15

Gly Leu Arg Gly Thr Gly Ser Asp Cys Pro Ala Leu Ala Gln Gln Gln
20 25 30

Thr Ala Leu Lys Asp Val Leu Gly Val Arg Asn Trp Ala Ser Ser Gly
35 40 45

Pro Phe Leu Leu Gly Leu Ser Leu Trp Arg Met Gly Trp Met Gly Glu
50 55 60

Lys Thr Gly Lys Ile Leu Thr Glu Phe Leu Gln Phe Tyr Glu Asp Gln
65 70 75 80

Tyr Gly Val Ala Leu Phe Asn Ser Met Arg His Glu Ile Glu Gly Thr
85 90 95

Gly Leu Pro Gln Ala Gln Leu Leu Trp Arg Lys Val Pro Leu Asp Glu
100 105 110

Arg Ile Val Phe Ser Gly Asn Leu Phe Gln His Gln Glu Asp Ser Lys
115 120 125

Lys Trp Arg Asn Arg Phe Ser Leu Val Pro His Asn Tyr Gly Leu Val
130 135 140

Leu Tyr Glu Asn Lys Ala Ala Tyr Glu Arg Gln Val Pro Pro Arg Ala
145 150 155 160

Val Ile Asn Ser Ala Gly Tyr Lys Ile Leu Thr Ser Val Asp Gln Tyr
165 170 175

Leu Glu Leu Ile Gly Asn Ser Leu Pro Gly Thr Thr Ala Lys Ser Gly
180 185 190

095-US1 sequ lstg.ST25.txt

Ser Ala Pro Ile Leu Lys Cys Pro Thr Gln Phe Pro Leu Ile Leu Trp
195 200 205

His Pro Tyr Ala Arg His Tyr Tyr Phe Cys Met Met Thr Glu Ala Glu
210 215 220

Gln Asp Lys Trp Gln Ala Val Leu Gln Asp Cys Ile Arg His Cys Asn
225 230 235 240

Asn Gly Ile Pro Glu Asp Ser Lys Val Glu Gly Pro Ala Phe Thr Asp
245 250 255

Ala Ile Arg Met Tyr Arg Gln Ser Lys Glu Leu Tyr Gly Thr Trp Glu
260 265 270

Met Leu Cys Gly Asn Glu Val Gln Ile Leu Ser Asn Leu Val Met Glu
275 280 285

Glu Leu Gly Pro Glu Leu Lys Ala Glu Leu Gly Pro Arg Leu Lys Gly
290 295 300

Lys Pro Gln Glu Arg Gln Arg Gln Trp Ile Gln Ile Ser Asp Ala Val
305 310 315 320

Tyr His Met Val Tyr Glu Gln Ala Lys Ala Arg Phe Glu Glu Val Leu
325 330 335

Ser Lys Val Gln Gln Val Gln Pro Ala Met Gln Ala Val Ile Arg Thr
340 345 350

Asp Met Asp Gln Ile Ile Thr Ser Lys Glu His Leu Ala Ser Lys Ile
355 360 365

Arg Ala Phe Ile Leu Pro Lys Ala Glu Val Cys Val Arg Asn His Val
370 375 380

Gln Pro Tyr Ile Pro Ser Ile Leu Glu Ala Leu Met Val Pro Thr Ser
385 390 395 400

Gln Gly Phe Thr Glu Val Arg Asp Val Phe Phe Lys Glu Val Thr Asp
405 410 415

Met Asn Leu Asn Val Ile Asn Glu Gly Gly Ile Asp Lys Leu Gly Glu
420 425 430

Tyr Met Glu Lys Leu Ser Arg Leu Ala Tyr His Pro Leu Lys Met Gln
435 440 445

095-US1 sequ lstg.ST25.txt

Ser Cys Tyr Glu Lys Met Glu Ser Leu Arg Leu Asp Gly Leu Gln Gln
450 455 460

Arg Phe Asp Val Ser Ser Thr Ser Val Phe Lys Gln Arg Ala Gln Ile
465 470 475 480

His Met Arg Glu Gln Met Asp Asn Ala Val Tyr Thr Phe Glu Thr Leu
485 490 495

Leu His Gln Glu Leu Gly Lys Gly Pro Thr Lys Glu Glu Leu Cys Lys
500 505 510

Ser Ile Gln Arg Val Leu Glu Arg Val Leu Lys Lys Tyr Asp Tyr Asp
515 520 525

Ser Ser Ser Val Arg Lys Arg Phe Phe Arg Glu Ala Leu Leu Gln Ile
530 535 540

Ser Ile Pro Phe Leu Leu Lys Lys Leu Ala Pro Thr Cys Lys Ser Glu
545 550 555 560

Leu Pro Arg Phe Gln Glu Leu Ile Phe Glu Asp Phe Ala Arg Phe Ile
565 570 575

Leu Val Glu Asn Thr Tyr Glu Glu Val Val Leu Gln Thr Val Met Lys
580 585 590

Asp Ile Leu Gln Ala Val Lys Glu Ala Ala Val Gln Arg Lys His Asn
595 600 605

Leu Tyr Arg Asp Ser Met Val Met His Asn Ser Asp Pro Asn Leu His
610 615 620

Leu Leu Ala Glu Gly Ala Pro Ile Asp Trp Gly Glu Glu Tyr Ser Asn
625 630 635 640

Ser Gly Gly Gly Ser Pro Ser Pro Ser Thr Pro Glu Ser Ala Thr
645 650 655

Leu Ser Glu Lys Arg Arg Arg Ala Lys Gln Val Val Ser Val Val Gln
660 665 670

Asp Glu Glu Val Gly Leu Pro Phe Glu Ala Ser Pro Glu Ser Pro Pro
675 680 685

Pro Ala Ser Pro Asp Gly Val Thr Glu Ile Arg Gly Leu Leu Ala Gln
690 695 700

095-US1 sequ lstg.ST25.txt

Gly Leu Arg Pro Glu Ser Pro Pro Pro Ala Gly Pro Leu Leu Asn Gly
705 710 715 720

Ala Pro Ala Gly Glu Ser Pro Gln Pro Lys Ala Ala Pro Glu Ala Ser
725 730 735

Ser Pro Pro Ala Ser Pro Leu Gln His Leu Leu Pro Gly Lys Ala Val
740 745 750

Asp Leu Gly Pro Pro Lys Pro Ser Asp Gln Glu Thr Gly Glu Gln Val
755 760 765

Ser Ser Pro Ser Ser His Pro Ala Leu His Thr Thr Thr Glu Asp Ser
770 775 780

Ala Gly Val Gln Thr Glu Phe
785 790